# **SCORE Search Results Details for Application** 09586625 and Search Result us-09-586-625-1.rng.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:

July 26, 2006, 12:11:09; Search time 3788 Seconds

(without alignments)

12567.717 Million cell updates/sec

Title:

US-09-586-625-1

Perfect score: 6828

Sequence:

1 gacggatcgggagatctccc.....gaaaagtgccacctgacgtc 6828

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched:

5244920 segs, 3486124231 residues

Total number of hits satisfying chosen parameters:

10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq\_8:\*

1: qeneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000s:\*

4: geneseqn2001as:\*

5: geneseqn2001bs:\* 6: geneseqn2002as:\*

7: geneseqn2002bs:\*

8: geneseqn2003as:\*

9: geneseqn2003bs:\*

10: geneseqn2003cs:\*

11: geneseqn2003ds:\*

12: geneseqn2004as:\*

13: geneseqn2004bs:\*

14: geneseqn2005s:\*

15: geneseqn2006s:\*

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OM nucleic - nucleic search, using sw model

Run on:

July 26, 2006, 13:23:40 ; Search time 28834 Seconds

(without alignments)

13241.909 Million cell updates/sec

Title:

US-09-586-625-1

Perfect score: 6828

Sequence:

1 gacqgatcgggagatctccc.....gaaaagtgccacctgacgtc 6828

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched:

48236798 segs, 27959665780 residues

Total number of hits satisfying chosen parameters:

96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est3:\*

3: gb\_est4:\*

4: gb\_est5:\*

5: gb est6:\*

6: gb htc:\*

7: gb est2:\*

8: qb est7:\*

9: gb est8:\* 10: gb\_est9:\*

11: gb gss1:\*

12: gb gss2:\*

13: gb gss3:\*

14: gb gss4:\*

Pred. No. is the number of results predicted by chance to have a

## **SCORE Search Results Details for Application** 09586625 and Search Result us-09-586-625-1.rni.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

July 26, 2006, 13:38:41; Search time 795 Seconds (without alignments)

16070.353 Million cell updates/sec

Title:

US-09-586-625-1

Perfect score: 6828

Sequence:

1 qacqqatcqqqaqatctccc.....gaaaagtgccacctgacgtc 6828

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched:

1403666 segs, 935554401 residues

Total number of hits satisfying chosen parameters:

2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:\*

1: /EMC Celerra SIDS3/ptodata/2/ina/1\_COMB.seq:\*

2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\* 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\* 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS COMB.seq:\*

8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*

9: /EMC Celerra SIDS3/ptodata/2/ina/RE COMB.seq:\*

10: /EMC Celerra SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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OM nucleic - nucleic search, using sw model

Run on:

July 26, 2006, 21:29:45; Search time 7306 Seconds

(without alignments)

11483.708 Million cell updates/sec

Title:

US-09-586-625-1

Perfect score: 6828

Sequence:

1 gacggatcgggagatctccc.....gaaaagtgccacctgacgtc 6828

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched:

18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters:

37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA Main:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq:\* /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq:\* 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\* 4: /EMC Celerra SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\* 5: /EMC Celerra SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\* 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\* 7: /EMC Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\* 8: /EMC Celerra SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\* 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\* 10: /EMC Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\* /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\* 11:

/EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\* /EMC Celerra SIDS3/ptodata/2/pubpna/US11A PUBCOMB.seq:\*

/EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq:\* /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq:\* 15:

/EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq:\*

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GenCore version 5.1.9
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```

OM nucleic - nucleic search, using sw model

July 26, 2006, 23:01:51; Search time 637 Seconds Run on:

(without alignments)

16384.827 Million cell updates/sec

Title: US-09-586-625-1

Perfect score: 6828

Sequence: 1 gacggatcgggagatctccc.....gaaaagtgccacctgacgtc 6828

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

2187952 segs, 764289321 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:\*

1: /EMC Celerra SIDS3/ptodata/2/pubpna/US09 NEW PUB.seq:\*

2: /EMC Celerra SIDS3/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*

3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*

4: /EMC Celerra SIDS3/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*

5: /EMC Celerra SIDS3/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*

8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq1:\*

9: /EMC Celerra SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result Query

Score Match Length DB ID Description

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16070.353 Million cell updates/sec

Title:

US-09-586-625-1

Perfect score: 6828

Sequence:

1 gacggatcgggagatctccc.....gaaaagtgccacctgacgtc 6828

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched:

1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters:

2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:\*

1: /EMC Celerra SIDS3/ptodata/2/ina/1\_COMB.seq:\* 2: /EMC Celerra SIDS3/ptodata/2/ina/5\_COMB.seq:\* 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\* 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*

6: /EMC Celerra SIDS3/ptodata/2/ina/H\_COMB.seq:\*

7: /EMC Celerra SIDS3/ptodata/2/ina/PCTUS\_COMB.seq:\*

8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\* 9: /EMC Celerra SIDS3/ptodata/2/ina/RE COMB.seq:\*

10: /EMC Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

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SUMMARIES